

09346470Results2

SEQ ID NO: 10

ALIGNMENTS

RESULT 1
097095
ID 097095 PRELIMINARY; PRT; 541 AA.
AC 097095;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ECDYSONE RECEPTOR.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FAT BODY;
RA Saleh D.S., Zhang J., Wyatt G.R., Walker V.K.;
RT "Cloning and characterization of an ecdysone receptor cDNA from
Locusta migratoria.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL; AF049136; AAD19828.1; -.
DR HSSP; P20393; 1A6Y.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Strdhormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECECTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
Zinc-finger.
SQ SEQUENCE 541 AA; 59197 MW; SC7A5ABD537F89CB CRC64:

Db 200 CKGFFRRSITKNAVYQCKYGNNCEIDMYMRRKCQECLKKCLTVGMRPECVVPEYCAVK 259
 Qy 305 RKEKKAQREKDKPNSTTDISPEIIKIEPTEMKIECGEPMIMGTPMPVTVPYVKPLSSEQKE 364
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 Db 260 RKEKKAQKDKDKPNSTTNGSPEVMLKDIDAKVEPERPLSNG-----IKPVSPEQEE 311
 |||||:|||:|||:|||:|||:
 Qy 365 LIHRLVYFQDQYEAPSEKDMKRLTINNQNMDYEDEEKQSDTTYRIITEMTILTVQLIVEF 424
 |||||:|||:|||:|||:
 Db 312 LIHRLVYFQNEYESPSEEDLRRVT----SQPTEGEDQSDVFRHITEITILTVQLIVEF 366
 |||||:
 Qy 425 AKRLPGFDKLVRDQITLLKACSSSEAMMFRVARKYDITTDISIVFANNQPFSAADSYNKAGL 484
 |||||:
 Db 367 AKRLPGFDKLLREDQIALLKACSSSEVMMFRMARRYDVNSDSILFANNQPYTKDSYNLAGM 426
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 Qy 485 GDAIENQLSFSRFMNMKVDNAEYALLTAIVIFSSRPNLLDGWVKEKIQEIYLESLKAYV 544
 |||:
 Db 427 GETIEDMLRFCRQMYAMKVDNAEYALLTAIVIFSERPSLVEGWVKEKIQEIYLEALKAYV 486
 |||:
 Qy 545 DNRDRDTATVRYARLLSVLTELRTLGNENSELCMTLKLKNRVPPFLAEIWVMP 599
 |||:
 Db 487 DNRRRPKSGTIFAKLLSVLTELRTLGNQNSEMCFSLKLKNKKLPPFLAEIWVIP 541

RESULT 2
 O02035
 ID 002035 PRELIMINARY; PRT; 491 AA.
 AC 002035;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE ECDYSONE RECEPTOR.
 GN ECR.
 OS Tenebrio molitor (Yellow mealworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 OC Cucujiformia; Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98000286; PubMed=9342239;
 RA Mouillet J.F., Delbecque J.P., Quennedey B., Delachambre J.;
 RT "Cloning of two putative ecdysteroid receptor isoforms from Tenebrio
 molitor and their developmental expression in the epidermis during
 metamorphosis.";
 RL Eur. J. Biochem. 248:856-863(1997).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
 DR EMBL; Y11533; CAA72296.1; -.
 DR HSSP; P20393; 1A6Y.
 DR InterPro; IPR000536; Hormone_rec_lig.
 DR InterPro; IPR000504; RRM.
 DR InterPro; IPR001723; Strdhormone_receptor.
 DR InterPro; IPR001628; zf-C4.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR SMART; SM00430; HOLI; 1.
 DR SMART; SM00399; ZnF_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECECTOR; 1.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
 KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
 KW Zinc-finger.
 SQ SEQUENCE 491 AA; 56096 MW; F997E90A56A789D1 CRC64;

Query Match 45.5%; Score 1434.5; DB 5; Length 491;
 Best Local Similarity 65.8%; Pred. No. 8.4e-99;
 Matches 293; Conservative 48; Mismatches 51; Indels 53; Gaps 9;

Qy 159 SPMMSGKIVKEELSPPNLSSGVSSHSGLKKKKLNHTPSTGVVNTSASGPGGVGNNVLNN 218

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Db    90 |||| :||| :||| :| :| |||| -----GP-----TP 121
Qy 219 RPPEELCLVCGDRSSGYHYNALTCEGCKGFFRSITKNAVYQCKYGNCEIDMYMRRKCQ 278
Db 122 RQQEELCLVCGDRASGYHYNALTCEGCKGFFRSITKNAVYQCKYGNCEIDMYMRRKCQ 181
Qy 279 ECRLKKCLTVGMRPECVVPEVQCAVKRKEKKAQREKDKPNSTTDISPEIIKIEP---TE 334
Db 182 ECRLKKCLSVGMRPECVVPEVQCAVKRKEKKAQKEKDKNSTNGSPDVKIEPELSDSE 241
Qy 335 MKIECGEPMIMGTPMPPTVPPVVKPLSEQKE--LIHRLVYFQDQYEAPSEKDMKRLTINNQ 392
Db 242 KTLTNGRNRI-----SPEQUEELILIHRLVYFQNNEYEHPSSEDVKR--IINQ 285
Qy 393 NMDEYDEEKQSDDTYRIITEMTILTQLIVEFAKRLPGFDKLVRDQITLLKACSSSEAMM 452
Db 286 PI---DGEDQCEIRFRHTTEITILTQLIVEFAKRLPGFDKLQEDQIALLKACSSEVMM 342
Qy 453 FRVARKYDITTD SIVFANNQPFSA DS YNKAGL GDAI ENQL SF SR FM YN MK VD N A E Y A L L T 512
Db 343 FRMARRYDVQSDSILFVN NN QPY PRD SYN LAG M GET IED LLH FC RT MYS M K VD N A E Y A L L T 402
Qy 513 AIVIFSSRPNLLDGWKVEKIQEIYLESLKAYVDNRDRDTATVRYARLLSVLTELRTLGNE 572
Db 403 AIVIFSERPSLIEGWKVEKIQEIYLEALRAYVDNRSPSRGTIFAKLLSVLTELRTLGNE 462
Qy 573 NSELCMTLKLKNR VPPPFLAEIWDV 597
Db 463 NSEM CISLKLKNKKLPPFLDEIWDV 487

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RESULT 3
O44337
ID O44337 PRELIMINARY; PRT; 560 AA.
AC O44337;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE AAMECRA1.
GN AAMECRA1.
OS Amblyomma americanum.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.
OX NCBI_TaxID=6943;
RN [1]
RP SEQUENCE FROM N.A.
RA Guo X., Harmon M.A., Laudet V., Mangelsdorf D.J., Palmer M.J.;
RL Insect Biochem. Mol. Biol. 0:0-0(1997).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL; AF020187; AAB94566.1; -.
DR HSSP; P20393; 1A6Y.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Strdhormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PRO0398; STRDHORMONER.
DR PRINTS; PRO0047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECECTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 560 AA; 61302 MW; 5054F2D2C037CD91 CRC64;

Query Match 42.6%; Score 1342.5; DB 5; Length 560;
Best Local Similarity 50.1%; Pred. No. 7.3e-92;
Matches 298; Conservative 71; Mismatches 133; Indels 93; Gaps 16;

Qy 23 GGVGGLMSYNRGRGGTEVIIKPRSPAVVQVATGGSYHGLPAASDAIVRSP-PGGHLPGP 81
 || ||| : | : | : | ; | : | ||| |||
 Db 37 GGAGGLAA----GSPPALSPNLPSSVVKVEP----RLP-----SPCVGGAASGD 76

 Qy 82 QQQVPPSRNGCSTLFSDIAGVKRLRPDDWLAVNSPPASSPGTSHIS-YTVISNGGGGGG 140
 ||| ||| ||| ||| ||| : | : | : |||
 Db 77 GGPVPP-----KRVQDDAGAWISSLPSQMSVGSLSPPPPLLNGVANSSG 121

 Qy 141 GGGGYNTSPMST-NSYDPYSPMSGKIVKEELSPPNLSGVSSH---SDGLKKKLNHTPS 196
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Db 122 -----LSPVSNCSYYDTYSRGP--CKEEMSPSSGGGLNGYFVDSFGDPKKKGAP- 172

 Qy 197 TGVVNTSASGPGGVGGNVLNNRPEECLCLVCGDRSSGYHYNALTCEGCKGFFRRSITKN 256
 | ||| ||| : ||| : ||| : ||| : ||| : ||| : |||
 Db 173 -----RQQEELCLVCGDRASGYHYNALTCEGCKGFFRRSITKN 210

 Qy 257 AVYQCKYGNNEIDMYMRRKCQECLKKCLTVGMRPECVVPEVQCAVKREKKAQREKDK 316
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Db 211 AVYQCKYGNNCIDIMYMRKCQECLKKCLSVGMRPECVVPEYQCAIKRESKKHQ--KDR 268

 Qy 317 PNSTTDISPEIIK-----IEPTEMKIECGEPIMGT-----PMPTVPYVKPLSSEQ 362
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Db 269 PNSTTRESPSALMAPSSVGGVSPTSQPMGGGSSLGSSNHEEDKKPVVLSPGVKPLSSQ 328

 Qy 363 KELIHLVYFQDQYEAPSEKDMKRLLTINNQNMDEYDEEKQSDTYRIITEMTILTVQLIV 422
 ::||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Db 329 EDLINKLVYYQQEFESPSEEDMKTT---PFPLGDSEEDNQRRFQHITEITILTVQLIV 384

 Qy 423 EFAKRLPGFDKLVRDQITLLKACSSSEAMMFRVARKYDITTD SIVFANNQPFSAWSYNA 482
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Db 385 EFSKRVPGFDTLAREDQITLLKACSSSEVMLRGARKYDVKTDSIVFANNQPYTRDNYRSA 444

 Qy 483 GLGDAIENQLSFSRFMYNMKVDNAEYALLTAIVFSSRPNLLDGWKVEKIQEIYLESLKA 542
 :||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Db 445 SVGDSADALFRFCRKMCQLRVDNAEYALLTAIVFSSRPLSVDPHKVERIQEYYIETLRM 504

 Qy 543 YVDNRDRDTATVRYARLLSVLTELRTLGNESELCMTLKLKNRVPFLAEIWDV 597
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 Db 505 YSENH-RPPGKNYFARLLSILTELRTLGNESELCMTLKLKNRVPFLAEIWDI 558

RESULT 4
 O44338
 ID O44338 PRELIMINARY; PRT; 570 AA.
 AC O44338;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE AAMECRA2.
 GN AAMECRA2.
 OS Amblyomma americanum.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.
 OX NCBI_TaxID=6943;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Guo X., Harmon M.A., Laudet V., Mangelsdorf D.J., Palmer M.J.;
 RL Insect Biochem. Mol. Biol. 0:0-0(1997).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
 DR EMBL; AF020188; AAB94567.1; -.
 DR HSSP; P20393; 1A6Y.
 DR InterPro; IPR000536; Hormone_rec_lig.
 DR InterPro; IPR001723; Strdhormone_receptor.
 DR InterPro; IPR001628; zf-C4.
 DR Pfam; PF00104; hormone_rec; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR SMART; SM00430; HOLI; 1.

DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECECTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 570 AA; 63127 MW; 1B0FAF391AA2033F CRC64;

RESULT 5
077240
ID 077240 PRELIMINARY; PRT; 513 AA.
AC 077240;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ECDYSONE RECEPTOR ISOFORM A.
GN ECR.
OS Choristoneura fumiferana (Spruce budworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidea; Tortricidae; Tortricinae; Choristoneura.
OX NCBI_TaxID=7141;
RN [1]
RP SEQUENCE FROM N.A.
RA Perera S.C., Ladd T.R., Dhadialla T.S., Krell P.J., Sohi S.S.,
RA Retnakaran A., Palli S.R.;
RT "Studies of two ecdysone receptor isoforms of the spruce budworm,

RT Choristoneura fumiferana.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDJB databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL; AF092030; AAC61596.2; -.
DR HSSP; P20393; 1A6Y.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Strdhormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECECTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 513 AA; 57621 MW; F110540A3030E602 CRC64;

RESULT 6
O44336
ID O44336 PRELIMINARY; PRT; 444 AA.
AC O44336;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE AAMECRA3.
GN AAMECRA3.

OS Amblyomma americanum.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Amblyomma.
OX NCBI_TaxID=6943;
RN [1]
RP SEQUENCE FROM N.A.
RA Guo X., Harmon M.A., Laudet V., Mangelsdorf D.J., Palmer M.J.;
RL Insect Biochem. Mol. Biol. 0:0-0(1997).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL; AF020186; AAB94565.1; -.
DR HSSP; P20393; 1A6Y.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Strdhormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PRO0398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 444 AA; 50283 MW; 3B087EEA29074DB7 CRC64;

Query Match 40.1%; Score 1265.5; DB 5; Length 444;
Best Local Similarity 55.9%; Pred. No. 2.9e-86;
Matches 255; Conservative 70; Mismatches 84; Indels 47; Gaps 9;

Qy	168	EELSPPNLSGVSSHSDGLKKKLHNTPSTGVVNTSASGPGGVGNNVLNN-----	218
Db	8	EDVPPPYT---AAAPEDFWRKEEM--SPSSG-----GGGLNGYFVDSFGDPKKKG	53
Qy	219	---RPPEELCLVCGDRSSGYHYNALTCEGCKGFRRSITKNAVYQCKYGNNCEIDMYMRR	275
Db	54	PAPRQQEELCLVCGDRASGYHYNALTCEGCKGFRRSITKNAVYQCKYGNNCIDDMYMR	113
Qy	276	KCQECLKKLTVGMRPECVVPEVQCAVKRKEKKAQREKDKNSTTDISPEI---	329
Db	114	KCQECLKKLTSVGMRPECVVPEYQCAIKRESKKHQ- -KDRPNSTTRRESPSALMAPSSVG	171
Qy	330	-IEPTEMKIECGEPMIMGT-----PMPTVPYVKPLSSEQKELIHLRLVYFQDQEYAPSE	381
Db	172	GVSPTSQPMGGGSSLGSSNHEEDKKPVVLSPGVKPLSSQEDLINKLVYYQQEFESPSE	231
Qy	382	KDMKRLTINNQNMDEYDEEKQSDDTYRIITEMTILTQVLIVEFAKRLPGFDKLVR	441
Db	232	EDMKKTT----PFPLGDSEEDNQRQFHITEITILTQVLIVEFSKRVPGFDTLAREDQIT	287
Qy	442	LLKACSSSEAMMFRVARKYDITTDISIVFANNQPFSA	501
Db	288	SSEVMMRLRGARKYDVKTDSIVFANNQPYTRDNYRSASVGDSADALFRFCRKM	347
Qy	502	KVDNAEYALLTAIVFSSRPNLLDGWVKEKIQEYI	561
Db	348	LESLKAYVDNRDRDTATVRYARLLS RVDNAEYALLTAIVFSSRPNLLDGWVKEKIQEYI	400
Qy	562	VLTELRTLGNENSELCMTLKLKNR	597
Db	407	VPPPFLAEIWV I	442

RESULT 7
076246
ID 076246 PRELIMINARY; PRT; 518 AA.
AC 076246;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE ECDYSTEROID RECEPTOR.
GN UPECR.
OS Uca pugilator (Atlantic sand fiddler crab) (Celuca pugilator).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Ocypodoidea; Ocypodidae; Ocypodinae; Uca complex; Celuca.
OX NCBI_TaxID=6772;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98368787; PubMed=9705089;
RA Chung A.C., Durica D.S., Clifton S.W., Roe B.A., Hopkins P.M.;
RT "Cloning of crustacean ecdysteroid receptor and retinoid-X receptor
RT gene homologs and elevation of retinoid-X receptor mRNA by retinoic
RT acid.";
RL Mol. Cell. Endocrinol. 139:209-227(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Durica D.S., Wu X., Anilkumar G., Hopkins P.M., Chung A.C.-K.;
RL Submitted (APR-2001) to the EMBL/GenBank/DDJB databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL; AF034086; AAC33432.2; -.
DR HSSP; P20393; 1A6Y.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001723; Strdhormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECECTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
FT VARIANT 261 266 AAPISP -> VAPISP.
SQ SEQUENCE 518 AA; 57408 MW; DD39B1F83753A878 CRC64;

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Qy  491 QLSFSRFMNYNMKVDNAEYALLTAIVFSSRPNLLDGWKVEKIQEIYLESLKAYVDNRD 550
     | : ||||||| || | || | : ||||:|||||:|||:|||
Db  409 LFRFCRSLCKMKVDNAEYALLAAIAIFSERPNLKEKKVKEQLQEIYLEALKSYVENRLP 468

Qy  551 TATVRYARLLSVLTELRTLGNENSELCMTLKLKNRVPVPPFLAEIWVD 597
     : : :||: :||| ||| ||| :| :||| : :||| ||| |
Db  469 RSNMVFAKLLNILTELRTLGNINSEMCFSLTLKNKRLLPPFLAEIWVD 515

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09346470Results

SEQ ID NO: 10

SUMMARIES

Result No.	Score	% Query			DB	ID	Description
		Match	Length	DB			
1	3152	100.0	599	22	AAB67101		M persicae ecdyson
2	2356	74.7	450	20	AAV28606		M. persicae EcR po
3	1246	39.5	546	21	AAV87470		European corn bore
4	1238	39.3	757	20	AAV28603		EcR polypeptide su
5	1238	39.3	757	22	AAB67096		L cuprina ecdysone
6	1224.5	38.8	757	19	AAW71297		Lucilia cuprina ec
7	1223	38.8	576	18	AAW06533		Heliothis ecdysone
8	1221	38.7	878	12	AAR13793		Ecdysone receptor.
9	1212	38.5	878	14	AAR32889		DHR23alpha protein
10	1171	37.2	746	18	AAW33655		Modified ecdysone
11	1160	36.8	746	21	AAV70357		Heterodimeric nucl
12	1155	36.6	764	21	AAV70358		Heterodimeric nucl
13	1149	36.5	746	18	AAW33654		Modified ecdysone
14	1131	35.9	1041	18	AAW33656		Modified ecdysone
15	1129.5	35.8	606	20	AAW95701		Bombyx mori nuclea
16	805	25.5	319	18	AAW06534		Spodoptera ecdyson
17	791	25.1	550	19	AAW45513		Ecdysone receptor
18	791	25.1	550	19	AAW39139		Drosophila ecdyson
19	791	25.1	550	21	AAV67558		Drosophila ecdyson
20	791	25.1	550	21	AAV78887		Ecdysone receptor
21	777	24.7	195	20	AAW28605		DNA-binding domain
22	777	24.7	195	22	AAB67100		M persicae ecdyson
23	731	23.2	445	21	AAV32374		Mouse CNREB-1. Mu
24	719.5	22.8	440	14	AAR33744		XR2. Homo sapiens
25	714	22.7	447	17	AAW03326		LXR-alpha, orphan
26	689.5	21.9	461	15	AAR52980		Human recombinant
27	689.5	21.9	461	17	AAR97982		Human steroid rece
28	689.5	21.9	461	17	AAR98140		NER receptor poten
29	684	21.7	460	16	AAR74738		Human ubiquitous n
30	682.5	21.7	461	17	AAR96234		Human foetal lung
31	682	21.6	460	18	AAW25034		Human ubiquitous n
32	678	21.5	446	17	AAR99736		Retinoid X recepto
33	678	21.5	484	17	AAR99735		Retinoid X recepto
34	673.5	21.4	443	16	AAR74739		Rat ubiquitous nuc
35	673.5	21.4	443	18	AAW25035		Rat ubiquitous nuc
36	671	21.3	446	17	AAR94169		OR-1 orphan recept
37	670	21.3	469	17	AAW03448		Farnesoid-activate
38	663.5	21.1	451	17	AAR99739		Retinoid X recepto
39	661	21.0	472	19	AAW40072		Human retinoid rec
40	648.5	20.6	477	22	AAE06680		Human nuclear horm
41	630.5	20.0	433	17	AAR88452		Retinoic acid rece
42	526.5	16.7	462	12	AAR10547		Murine Retinoic Ac
43	526.5	16.7	462	16	AAR84724		Murine retinoic ac
44	520.5	16.5	462	13	AAR27534		RAR-alpha protein.
45	520.5	16.5	462	16	AAR68023		RAR-alpha. Homo s

ALIGNMENTS

```

RESULT      1
AAB67101
ID   AAB67101 standard; Protein; 599 AA.
XX
AC   AAB67101;
XX
DT   10-APR-2001 (first entry)
XX
DE   M persicae ecdysone receptor EcR subunit SEQ ID NO: 14.
XX
KW   Insect; steroid hormone receptor; juvenile hormone receptor; fly;

```

KW EcR subunit; USP subunit; insecticide.
XX
OS Myzus persicae.
XX
PN WO200102436-A1.
XX
PD 11-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-AU00799.
XX
PR 01-JUL-1999; 99US-0346470.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Hill RJ, Hannan GN;
XX
DR WPI; 2001-080981/09.
DR N-PSDB; AAF32137.
XX
PT New nucleic acid molecule for the regulation of gene expression in
PT insects -
XX
PS Claim 1; Page 141-144; 172pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC Bemisia tabaci (Silverleaf whitefly), Myzus persicae (aphid) and Lucilia
CC cuprina (sheep blowfly) steroid and juvenile hormone steroid receptor
CC subunits EcR and USP. These can be used to screen for agents with
CC insecticidal activity.
XX
SQ Sequence 599 AA;

Query Match 100.0%; Score 3152; DB 22; Length 599;
Best Local Similarity 100.0%; Pred. No. 4.6e-231;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMDQKCDVGGGVAAAAAGIGGGVGGLMSYNRGRGGTEVIIKPRSPAVVQVATGGSYHG 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 mmdqkcdvgggvaaaaagigggvgglmsynrgrggteviikprspavvqvatggsyhg 60

Qy 61 LPAASDAIVRSPPGGHLPGPQQQVPPSRNGCSTLFSIDAGVKRLRPDDWLAVNSPPASS 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 lpaasdavivrsppgghlpgpqqqvppsrngcstlfsdiagvkrlrpddwlavnspass 120

Qy 121 PGTSIHISYTVISNGGGGGGGGGGYNTSPMSTNSYDPYSPMSGKIVKEELSPPNLSGV 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 pgtshisytvisnggggggggggyntspmstnsydpyspmmsgkivkeelspnslsgvs 180

Qy 181 SHSDGLKKKLNHTPSTGVVNTSASGPGGVGNNVLNNRPEELCLVCGDRSSGYHYNAL 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 shsdglkkknhtpstgvvntsasgpggvggnvlnnrppeelclvcgdrssgyhynal 240

Qy 241 TCEGCKGFFRRSITKNNAVYQCKYGNNEIDMYMRRKCQECLRKKCLTVGMRPECVVPEVQ 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 tcegckgffrrsиткнавуqckygnneidmymrrkcqeclkkcltvgmрречvvpevq 300

Qy 301 CAVKRKEKKAQREKDKPNSTTDISPEIICKIEPTEMKIECGEPIMGTPMPYVVKPLSS 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 cavkrkekkaqrekdkpnsttdispeiikieptemkiecgepmimgtppmptyvkplss 360

Qy 361 EQKELIHLVYFQDQYEAPSEKDMKRLTINNQNMDEYDEEKQSDTTYRIITEMTILTVQL 420
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 eqkelihrlvyfqdqeapsekdmkrltinnqnmdeydeekqsdttyriitemtiltvql 420

Qy 421 IVEFAKRLPGFDKLVRDQITLLKACSSSEAMMFRAVARYDITTDISVFAFNQPFSA 480
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 ivefakrlpgfdklvredqitllkacsseammfrvarkydittdsivfannqpfadsyn 480

Qy 481 KAGLGDAIENQLSFSRFMYNMKVDNAEYALLTAIVIFSSRPNLLDGWKVEKIQEYLES 540
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 481 kaglgdaienqlsfsrfmynmkvdnaeyalltaivifssrpnlldgwkvekiqeiylesl 540
 Qy 541 KAYVDNRDRDTATVRYARLLSVLTELRTLGNENSELCMTLKLKNRVPFFLAEIWDVMP 599
 |||||||
 Db 541 kayvdnrdrtatvryarllsvltelrtlgnenselcmtlklnrvppflaeiwdvmp 599

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1160	36.8	746	3	US-09-144-759-18	Sequence 18, Appli
2	1155	36.6	764	3	US-09-144-759-20	Sequence 20, Appli
3	1129.5	35.8	606	4	US-08-891-298-3	Sequence 3, Appli
4	791	25.1	550	3	US-08-659-188-18	Sequence 18, Appli
5	791	25.1	550	3	US-08-655-227-18	Sequence 18, Appli
6	791	25.1	550	3	US-08-655-241-18	Sequence 18, Appli
7	725.5	23.0	440	1	US-08-333-358-8	Sequence 8, Appli
8	725.5	23.0	440	1	US-08-463-694-8	Sequence 8, Appli
9	725.5	23.0	440	1	US-08-694-501-8	Sequence 8, Appli
10	714	22.7	447	1	US-08-373-935-1	Sequence 1, Appli
11	689.5	21.9	461	1	US-08-330-518-2	Sequence 2, Appli
12	689.5	21.9	461	1	US-08-330-283-2	Sequence 2, Appli
13	689.5	21.9	461	2	US-08-646-248-2	Sequence 2, Appli
14	689.5	21.9	461	5	PCT-US95-13924-2	Sequence 2, Appli
15	689.5	21.9	461	5	PCT-US95-13931-2	Sequence 2, Appli
16	682	21.6	460	1	US-08-342-411A-2	Sequence 2, Appli
17	678	21.5	446	2	US-08-372-652-3	Sequence 3, Appli
18	678	21.5	446	5	PCT-US95-16311-3	Sequence 3, Appli
19	678	21.5	484	2	US-08-372-652-1	Sequence 1, Appli
20	678	21.5	484	5	PCT-US95-16311-1	Sequence 1, Appli
21	673.5	21.4	443	1	US-08-342-411A-4	Sequence 4, Appli
22	671	21.3	446	4	US-08-776-844-2	Sequence 2, Appli
23	670	21.3	469	3	US-08-372-183-2	Sequence 2, Appli
24	670	21.3	469	4	US-09-469-721-2	Sequence 2, Appli
25	670	21.3	469	5	PCT-US95-17023-2	Sequence 2, Appli
26	663.5	21.1	451	2	US-08-372-652-2	Sequence 2, Appli
27	663.5	21.1	451	5	PCT-US95-16311-2	Sequence 2, Appli
28	661	21.0	472	1	US-08-496-631-2	Sequence 2, Appli
29	630.5	20.0	433	2	US-08-466-120-2	Sequence 2, Appli
30	630.5	20.0	433	5	PCT-US94-07266-2	Sequence 2, Appli
31	520.5	16.5	462	2	US-08-592-383-2	Sequence 2, Appli
32	520.5	16.5	462	2	US-08-095-728B-4	Sequence 4, Appli
33	520.5	16.5	462	5	PCT-US92-02320A-4	Sequence 4, Appli
34	515	16.3	403	2	US-08-592-383-4	Sequence 4, Appli
35	514.5	16.3	454	4	US-08-764-870-5	Sequence 5, Appli
36	514.5	16.3	454	4	US-08-980-115-5	Sequence 5, Appli
37	514.5	16.3	454	6	5260432-2	Patent No. 5260432
38	509.5	16.2	462	6	5171671-2	Patent No. 5171671
39	495.5	15.7	410	4	US-08-764-870-1	Sequence 1, Appli
40	495.5	15.7	410	4	US-08-980-115-1	Sequence 1, Appli
41	495	15.7	410	4	US-08-764-870-2	Sequence 2, Appli
42	495	15.7	410	4	US-08-980-115-2	Sequence 2, Appli
43	495	15.7	410	6	5438126-2	Patent No. 5438126
44	489	15.5	448	6	5223606-2	Patent No. 5223606
45	483	15.3	461	4	US-08-764-870-3	Sequence 3, Appli



SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	1224	38.8	878	2	A41055	ecdysone receptor
2	1159	36.8	536	2	A56590	ecdysteroid recept

3	726	23.0	445	2	A56043	steroid hormone re
4	714	22.7	447	2	I38975	nuclear orphan rec
5	689.5	21.9	461	2	JC4014	steroid hormone-nu
6	678	21.5	469	2	A56918	farnesoid x-activa
7	678	21.5	484	2	I49018	retinoid X recepto
8	677	21.5	446	2	I49021	retinoid X recepto
9	671	21.3	446	2	I59354	orphan nuclear rec
10	567.5	18.0	379	2	I49020	retinoid X recepto
11	539.5	17.1	476	2	B41977	retinoic acid rece
12	526.5	16.7	462	2	S05050	retinoic acid nucl
13	523.5	16.6	338	2	I49019	retinoid X recepto
14	523.5	16.6	458	2	S06123	retinoic acid rece
15	520.5	16.5	462	1	A29491	retinoic acid rece
16	517.5	16.4	458	2	A34714	retinoic acid rece
17	515	16.3	442	2	A38592	retinoic acid rece
18	514.5	16.3	454	1	A33903	retinoic acid rece
19	511.5	16.2	418	2	B36067	thyroid hormone re
20	511	16.2	444	2	I51256	retinoic acid rece
21	510	16.2	499	2	I51257	retinoic acid rece
22	510	16.2	955	4	C40045	probable transcrip
23	509.5	16.2	443	1	C35991	retinoic acid rece
24	509.5	16.2	447	2	B34714	retinoic acid rece
25	507	16.1	455	2	S13512	retinoic acid rece
26	506.5	16.1	418	1	TVXLTA	thyroid hormone re
27	504.5	16.0	454	2	S06124	retinoic acid rece
28	502	15.9	408	1	TVCHVR	thyroid hormone re
29	499	15.8	459	2	A41977	retinoic acid rece
30	498.5	15.8	410	2	S14416	thyroid hormone re
31	498	15.8	453	2	I50674	retinoic acid rece
32	496.5	15.8	410	1	QRMSA1	thyroid hormone re
33	496	15.7	373	2	I51165	gene c-erbA-beta p
34	495.5	15.7	410	2	S09178	thyroid hormone re
35	495.5	15.7	448	2	A43786	retinoic acid rece
36	495	15.7	373	2	D36067	thyroid hormone re
37	495	15.7	373	2	C36067	thyroid hormone re
38	495	15.7	410	2	A40917	thyroid hormone re
39	492	15.6	369	1	TVCHTB	thyroid hormone re
40	492	15.6	369	2	S58211	beta-thyroid hormo
41	488	15.5	448	2	S02827	retinoic acid rece
42	487	15.5	464	2	A56558	retinoic acid rece
43	485.5	15.4	410	2	S06410	thyroid hormone re
44	485.5	15.4	452	2	S78481	retinoic acid rece
45	484	15.4	448	2	S05051	retinoic acid rece

SUMMARIES

Result No.	Query				Description
	Score	Match	Length	DB ID	
1	1238	39.3	757	1 ECR_LUCCU	O18531 lucilia cup
2	1224	38.8	878	1 ECR_DROME	P34021 drosophila
3	1223	38.8	576	1 ECR_HELV1	O18473 heliothis v
4	1218	38.6	675	1 ECR_AEDAE	P49880 aedes aegyp
5	1198	38.0	556	1 ECR_MANSE	P49883 manduca sex
6	1159	36.8	536	1 ECR_CHITE	P49882 chironomus
7	1129.5	35.8	606	1 ECR_BOMMO	P49881 bombyx mori
8	731	23.2	445	1 NRH3_MOUSE	Q9z0y9 mus musculu
9	726	23.0	445	1 NRH3_RAT	Q62685 rattus norv
10	714	22.7	447	1 NRH3_HUMAN	Q13133 homo sapien
11	689.5	21.9	461	1 NRH2_HUMAN	P55055 homo sapien
12	677	21.5	446	1 NRH2_MOUSE	Q60644 mus musculu
13	671	21.3	446	1 NRH2_RAT	Q62755 rattus norv
14	539.5	17.1	476	1 RRG1_XENLA	P51127 xenopus lae
15	526.5	16.7	462	1 RRA_MOUSE	P11416 mus musculu
16	523.5	16.6	458	1 RRA_NOTVI	P18514 notophthalm
17	520.5	16.5	462	1 RRA_HUMAN	P10276 homo sapien

18	517.5	16.4	427	1	THA1_BRARE	Q98867 brachydanio
19	517.5	16.4	458	1	RRG1_MOUSE	P18911 mus musculu
20	515	16.3	442	1	RRG2_XENLA	P28699 xenopus lae
21	514.5	16.3	454	1	RRG1_HUMAN	P13631 homo sapien
22	513.5	16.3	418	1	THAB_XENLA	P18115 xenopus lae
23	510	16.2	499	1	RRG_BRARE	Q91392 brachydanio
24	509.5	16.2	443	1	RRG2_HUMAN	P22932 homo sapien
25	509.5	16.2	447	1	RRG2_MOUSE	P20787 mus musculu
26	506.5	16.1	416	1	THA_SALSA	Q9w785 salmo salar
27	506	16.1	455	1	RRB_CHICK	P22448 gallus gall
28	505	16.0	505	1	RRG_NOTVI	P18516 notophthalm
29	503.5	16.0	418	1	THAA_XENLA	P15204 xenopus lae
30	503.5	16.0	418	1	THA_RANCA	Q02777 rana catesb
31	502	15.9	408	1	THA_CHICK	P04625 gallus gall
32	499	15.8	401	1	THA_CAIMO	Q90382 cairina mos
33	499	15.8	414	1	THBB_XENLA	P18119 xenopus lae
34	496	15.7	373	1	THB_RANCA	Q02965 rana catesb
35	496	15.7	386	1	THB_BRARE	Q9pve4 brachydanio
36	495	15.7	373	1	THBA_XENLA	P18117 xenopus lae
37	495	15.7	410	1	THA1_SHEEP	Q28570 ovis aries
38	493.5	15.7	395	1	THB_PAROL	Q91279 paralichthy
39	493.5	15.7	458	1	RRA_XENLA	P51126 xenopus lae
40	492	15.6	369	1	THB_CHICK	P18112 gallus gall
41	491	15.6	402	1	THA_APTPA	O42295 aptenodytes
42	488	15.5	448	1	RRB2_HUMAN	P10826 homo sapien
43	487.5	15.5	482	1	RRB_MOUSE	P22605 mus musculu
44	486	15.4	476	1	THB2_HUMAN	P37243 homo sapien
45	483.5	15.3	416	1	THA_HIPHI	Q9w6n4 hippoglossu

SUMMARIES

%

Result No.	Query				Description
	Score	Match	Length	DB ID	
1	1613.5	51.2	541	5 097095	097095 locusta mig
2	1434.5	45.5	491	5 002035	002035 tenebrio mo
3	1342.5	42.6	560	5 044337	044337 amblyomma a
4	1312.5	41.6	570	5 044338	044338 amblyomma a
5	1293.5	41.0	513	5 077240	077240 choristoneu
6	1265.5	40.1	444	5 044336	044336 amblyomma a
7	1258	39.9	518	5 076246	076246 uca pugilat
8	1233.5	39.1	673	5 076827	076827 ceratitis c
9	1231.5	39.1	881	5 Q9V9K8	Q9v9k8 drosophila
10	1221.5	38.8	784	5 Q9GPH1	Q9gph1 calliphora
11	1219	38.7	680	5 Q9U3Y4	Q9u3y4 aedes albop
12	1217.5	38.6	541	5 077255	077255 choristoneu
13	937	29.7	339	5 Q9U0R9	Q9u0r9 junonia coe
14	937	29.7	346	5 Q9U3U4	Q9u3u4 bicyclus an
15	678	21.5	469	11 Q62735	Q62735 rattus norv
16	678	21.5	484	11 Q60641	Q60641 mus musculu
17	661	21.0	472	4 Q92943	Q92943 homo sapien
18	584.5	18.5	207	5 Q9XYR8	Q9xyr8 bradysia hy
19	567.5	18.0	379	11 Q60643	Q60643 mus musculu
20	539.5	17.1	460	13 Q90966	Q90966 gallus gall
21	523.5	16.6	338	11 Q60642	Q60642 mus musculu
22	523	16.6	446	13 Q9I8T2	Q9i8t2 ambystoma m
23	520.5	16.5	462	11 P97513	P97513 mus spretus
24	519.5	16.5	441	13 Q9I8T3	Q9i8t3 ambystoma m
25	517.5	16.4	462	4 P78456	P78456 homo sapien
26	517	16.4	444	13 Q90271	Q90271 brachydanio
27	511	16.2	444	13 Q91391	Q91391 brachydanio
28	505.5	16.0	447	13 Q9W5Z3	Q9w5z3 fugu rubrip
29	504	16.0	455	13 Q9W6B3	Q9w6b3 coturnix co
30	503.5	16.0	454	13 Q9W5Z4	Q9w5z4 fugu rubrip
31	498.5	15.8	582	12 Q96593	Q96593 avian eryth
32	498	15.8	453	13 Q90967	Q90967 gallus gall

33	497	15.8	426	13	Q90968	Q90968 gallus gall
34	497	15.8	434	5	P91780	P91780 polyandroca
35	495.5	15.7	457	13	Q90272	Q90272 brachydanio
36	491.5	15.6	381	4	Q9UJ38	Q9uj38 homo sapien
37	488	15.5	459	11	Q9QWJ1	Q9qwj1 rattus norv
38	485.5	15.4	452	13	Q91155	Q91155 notophthalm
39	482	15.3	182	5	Q9NGU6	Q9ngu6 sarcophaga
40	482	15.3	416	4	Q9P300	Q9p300 homo sapien
41	482	15.3	555	12	O36200	O36200 avian eryth
42	482	15.3	797	4	Q15156	Q15156 homo sapien
43	477	15.1	448	13	Q92019	Q92019 xenopus lae
44	474	15.0	555	12	Q96594	Q96594 avian eryth
45	469.5	14.9	455	12	Q85511	Q85511 avian eryth

SEQ ID NO: 9, Oligo Search

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	33	1.8	306250	1	SME591788	AL591788 Sinorhizo
2	30	1.7	2512	9	CHPRGITX	M30950 Chimpanzee
c 3	30	1.7	2832	14	SLMNPVRR	X98924 Spodoptera
c 4	30	1.7	131673	9	HS336H9	AL031224 Human DNA
5	30	1.7	169505	9	CNS01DTV	AL132987 Human chr
c 6	29	1.6	1800	8	VCPHEROPH	Y07752 V.carteri m
c 7	29	1.6	63179	2	AC090435	AC090435 Chlamydom
8	29	1.6	99799	2	AC090436	AC090436 Chlamydom
9	29	1.6	131824	2	AP004037	AP004037 Oryza sat
c 10	29	1.6	235302	2	AC073784	AC073784 Mus muscu
11	28	1.6	2850	6	AR058199	AR058199 Sequence
12	28	1.6	3700	9	HSPILOT	Y07558 H.sapiens P
13	28	1.6	4272	9	HSPILMRNA	X63741 H.sapiens p
14	28	1.6	4289	9	S40832	S40832 EGR3=EGR3 p
c 15	28	1.6	181874	2	AC055854	AC055854 Homo sapi
16	27	1.5	780	7	AF349975	AF349975 Bacteriop
17	27	1.5	110000	2	LMFLCHR16_08	Continuation (9 of
18	27	1.5	195859	14	AF281817	AF281817 Tupaia he
c 19	26	1.4	452	10	MUSPKCDB	M21096 Mouse cAMP-
20	26	1.4	1714	7	MYM1G38	X05676 Bacteriopha
21	26	1.4	2295	10	MMU300577	AJ300577 Mus muscu
c 22	26	1.4	4591	9	AB014534	AB014534 Homo sapi
c 23	26	1.4	147203	8	AP003687	AP003687 Oryza sat
24	26	1.4	209157	9	CNS01DW4	AL136332 Human chr
25	26	1.4	294800	1	SME591789	AL591789 Sinorhizo
26	25	1.4	320	3	AF170287	AF170287 Gnamptoge
27	25	1.4	1023	7	PRD1CAPV	M55568 Bacteriopha
28	25	1.4	1074	1	AF198618	AF198618 Streptomy
29	25	1.4	1938	10	AF038538	AF038538 Mus muscu
c 30	25	1.4	2544	8	ZMAHAS109	X63554 Z.mays gene
31	25	1.4	4130	3	AF210733	AF210733 Aedes alb
32	25	1.4	4158	3	AAU02021	U02021 Aedes aegyp
33	25	1.4	12387	10	AF038537	AF038537 Mus muscu
34	25	1.4	14925	7	PRDCG	M69077 Bacteriopha
35	25	1.4	28825	10	AF093624	AF093624 Mus muscu
36	25	1.4	86538	2	AC008238	AC008238 Arabidops
c 37	25	1.4	89219	8	ATT6K22	AL031187 Arabidops
c 38	25	1.4	95266	8	ATF18E5	AL022603 Arabidops
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c 40	25	1.4	110000	2	LMFLCHR25_04	Continuation (5 of
41	25	1.4	110000	2	LMFLCHR34_14	Continuation (15 o
42	25	1.4	128413	14	NPHT3COMP	L33180 Bombyx mori
43	25	1.4	150378	2	AP003291	AP003291 Oryza sat
44	25	1.4	163055	2	AP003626	AP003626 Oryza sat
c 45	25	1.4	194916	8	ATCHRIV55	AL161555 Arabidops

ALIGNMENTS

RESULT 1
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 LOCUS SME591788 306250 bp DNA BCT 16-AUG-2001
 DEFINITION Sinorhizobium meliloti 1021 complete chromosome; segment 7/12.
 ACCESSION AL591788 AL591688
 VERSION AL591788.1 GI:15074579
 KEYWORDS
 SOURCE Sinorhizobium meliloti.
 ORGANISM Sinorhizobium meliloti
 Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 Rhizobiaceae; Sinorhizobium.
 REFERENCE 1 (bases 1 to 306250)
 AUTHORS Capela,D., Barloy-Hubler,F., Gouzy,J., Bothe,G., Ampe,F., Batut,J.,
 Boistard,P., Becker,A., Boutry,M., Cadieu,E., Dreano,S., Gloux,S.,
 Godrie,T., Goffeau,A., Kahn,D., Kiss,E., Lelaure,V., Masuy,D.,
 Pohl,T., Portetelle,D., Puebler,A., Purnelle,B., Ramsperger,U.,
 Renard,C., Thebault,P., Vandembol,M., Weidner,S. and Galibert,F.
 TITLE From the Cover: Analysis of the chromosome sequence of the legume
 symbiont Sinorhizobium meliloti strain 1021
 JOURNAL Proceedings of the National Academy of Sciences of the United
 States of America. 98 (17), 9877-9882 (2001)
 PUBMED 11481430
 REFERENCE 2 (bases 1 to 306250)
 AUTHORS Gouzy,J.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUL-2001) Gouzy J., Submitted on behalf of the MELILO
 EU Consortium
 COMMENT MELILO EU Consortium:
 Laboratoire de Biologie Moleculaire des Relations
 Plantes-Microorganismes, UMR215-CNRS-INRA, BP27, F-31326 Castanet,
 France, Laboratoire de Genetique et Developpement UMR6061-CNRS,
 Faculte de Medecine, 2 avenue du Pr. Leon Bernard, F-35043 Rennes,
 France, GATC GmbH, Fritz-Arnold-str. 23, D-78467 Konstanz, Germany,
 Universitaet Bielefeld, Biologie IV (Genetik) Universitaetstr 25,
 D-33615 Bielefeld, Germany, Unite de Biochimie physiologique,
 Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20,
 B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Faculte
 des Sciences Agronomiques de Gembloux, Avenue Marechal Juin 6,
 B-5030 Gembloux, Belgium. E-mail:Jerome.Gouzy@toulouse.inra.fr
<http://sequence.toulouse.inra.fr/meliloti.html>.
 FEATURES Location/Qualifiers
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Db 277983 CGGCAGCGGCGGTGGCGCGGTGGCGCGGTGG 278015

RESULT 2
CHPRGITX
LOCUS CHPRGITX 2512 bp DNA PRI 27-APR-1993
DEFINITION Chimpanzee 28S ribosomal RNA gene fragment.
ACCESSION M30950
VERSION M30950.1 GI:176891
KEYWORDS 28S ribosomal RNA.
SOURCE Chimpanzee DNA.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 2512)
AUTHORS Gonzalez,I.L., Sylvester,J.E., Smith,T.F., Stambolian,D. and
Schwickel,R.D.
JOURNAL Unpublished
REFERENCE 2 (bases 193 to 261; 375 to 945; 1042 to 1079; 1334 to 1357; 1742
to 1958; 2190 to 2204)
AUTHORS Gonzalez,I.L., Sylvester,J.E., Smith,T.F., Stambolian,D. and
Schwickel,R.D.
TITLE Ribosomal RNA gene sequences and hominoid phylogeny
JOURNAL Mol. Biol. Evol. 7, 203-219 (1990)
MEDLINE 90294723
COMMENT Draft entry and computer-readable sequence for [2], [1] kindly
submitted by I.L.Gonzalez, 20-DEC-1989.
FEATURES Location/Qualifiers
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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SUMMARIES

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	2	1350	75.1	1353	20	AAX90669
	3	424	23.6	585	20	AAX90668
	4	424	23.6	585	22	AAF32134
c	5	28	1.6	379	21	AAC56804
	6	28	1.6	2850	20	AAV64278
	7	23	1.3	23	20	AAX90678
	8	23	1.3	23	22	AAF32146
	9	23	1.3	208	20	AAX90672
	10	23	1.3	208	22	AAF32135
c	11	23	1.3	2822	22	AAH24912
	12	22	1.2	1677	17	AAT31932
	13	22	1.2	1787	17	AAT31928
	14	22	1.2	48300	22	AAF61281
	15	21	1.2	76	21	AAC17910
	16	21	1.2	126	15	AAQ73442
c	17	21	1.2	300	21	AAA35327
	18	21	1.2	800	22	AAH03632
	19	21	1.2	1028	13	AAQ27091
	20	21	1.2	1028	22	AAA91542

21	21	1.2	1028	22	AAS01347	Human Fragile X Sy
c 22	21	1.2	1414	22	AAH17027	Human cDNA sequenc
23	21	1.2	1601	22	AAH13799	Human cDNA sequenc
24	21	1.2	1608	21	AAZ22298	Human potassium ch
c 25	21	1.2	2036	19	AAV29540	Homo sapiens D8725
c 26	21	1.2	2075	18	AAT75444	CDNA encoding oste
c 27	21	1.2	2205	19	AAV04680	Human presenilin i
c 28	21	1.2	2430	16	AAQ83161	DNA encoding malic
c 29	21	1.2	3517	17	AAT31287	Rabbit poly-immuno
30	21	1.2	5820	18	AAT71205	HaSNPV polyhedrin
31	21	1.2	6530	14	AAQ51557	Loricrin gene. Ho
32	21	1.2	6530	20	AAZ22072	Nucleotide sequenc
33	21	1.2	6530	22	AAC68948	Mouse loricrin gen
34	21	1.2	7860	17	AAT44380	Stretch-activated
35	21	1.2	8601	13	AAQ24828	AFP-1. Homo sapie
36	21	1.2	8601	13	AAQ24829	AFP-1 (C 7508 T).
c 37	21	1.2	9997	18	AAT97925	Composite sequence
c 38	21	1.2	9997	19	AAV05839	Mouse huntingtin c
39	20	1.1	87	21	AAA05701	Oligonucleotide SE
c 40	20	1.1	111	14	AAQ39031	Oligonucleotide id
c 41	20	1.1	115	14	AAQ39033	Oligonucleotide id
42	20	1.1	452	22	AAF68087	Human lung tumour
43	20	1.1	1289	22	AAF75749	Rice MADS box gene
c 44	20	1.1	1371	18	AAT78974	Mouse Huntington's
45	20	1.1	1491	20	AAX15147	Nucleotide sequenc

ALIGNMENTS

RESULT 1
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 ID AAF32137 standard; cDNA; 1797 BP.
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 AC AAF32137;
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 DT 10-APR-2001 (first entry)
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 KW Insect; steroid hormone receptor; juvenile hormone receptor; fly;
 KW EcR subunit; USP subunit; insecticide; ss.
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 OS Myzus persicae.
 XX
 PN WO200102436-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-AU00799.
 XX
 PR 01-JUL-1999; 99US-0346470.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Hill RJ, Hannan GN;
 XX
 DR WPI; 2001-080981/09.
 DR P-PSDB; AAB67101.
 XX
 PT New nucleic acid molecule for the regulation of gene expression in
 PT insects -
 XX
 PS Claim 23; Page 138-141; 172pp; English.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC Bemisia tabaci (Silverleaf whitefly), Myzus persicae (aphid) and Lucilia
 CC cuprina (sheep blowfly) steroid and juvenile hormone steroid receptor
 CC subunits EcR and USP. These can be used to screen for agents with
 CC insecticidal activity.
 XX

SQ Sequence 1797 BP; 512 A; 444 C; 459 G; 382 T; 0 other;

Query Match 100.0%; Score 1797; DB 22; Length 1797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1081 gaacaaaaagaactgatccaccgacttgtctattccaggatcaatatgaagtcctag 1140
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Qy      1201 aaacaaagtgacaccacatatcgaaatcatcactgagatgacaataactcacagttcaactg 1260
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Qy      1261 attgttagttgc当地aaacgattaccagggtttcgataaaacttgc当地aaatggatcaatc 1320
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db      1261 attgttagttgc当地aaacgattaccagggtttcgataaaacttgc当地aaatggatcaatc 1320

Qy      1321 actttactcaaggctgtcaagtgaagtatgatgttc当地ggatcaaggaaatgtac 1380
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db      1321 actttactcaaggctgtcaagtgaagtatgatgttc当地ggatcaaggaaatgtac 1380

Qy      1381 atcaccactgactcaatagtgtttgctaacaaccaggccatttc当地gttcatataac 1440
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db      1381 atcaccactgactcaatagtgtttgctaacaaccaggccatttc当地gttcatataac 1440

Qy      1441 aaagctggattggagatgccattgaaaccaactgtcattc当地gttcatataat 1500
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db      1441 aaagctggattggagatgccattgaaaccaactgtcattc当地gttcatataat 1500

Qy      1501 atgaaggtaggataacgc当地aaatgc当地attgaccgc当地atcgatatttc当地gttagg 1560
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db      1501 atgaaggtaggataacgc当地aaatgc当地attgaccgc当地atcgatatttc当地gttagg 1560

Qy      1561 ccaaatttactagatgttggaaagtgagaaatccaaggaaatctacatgtatgc当地ttta 1620
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db      1561 ccaaatttactagatgttggaaagtgagaaatccaaggaaatctacatgtatgc当地ttta 1620

Qy      1621 aaagcttatgttagataatcgagaccgtgacacagcaactgtacgatatgc当地gttctc 1680
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db      1621 aaagcttatgttagataatcgagaccgtgacacagcaactgtacgatatgc当地gttctc 1680

Qy      1681 tcagtagttacagaattgc当地ccataggcaatgaaactctgagatgtatgc当地actg 1740
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db      1681 tcagtagttacagaattgc当地ccataggcaatgaaactctgagatgtatgc当地actg 1740

Qy      1741 aaactgaaaaacagagatgtacccattttggccgaaatatggatgtatgcca 1797
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db      1741 aaactgaaaaacagagatgtacccattttggccgaaatatggatgtatgcca 1797

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RESULT      2
AAX90669
ID   AAX90669 standard; cDNA; 1353 BP.
XX
AC   AAX90669;
XX
DT   11-OCT-1999 (first entry)
XX
DE   M. persicae ecdysone receptor EcR polypeptide subunit full-length cDNA.
XX

```

KW Myzus persicae EcR polypeptide subunit full-length cDNA; aphid;
KW hemipteran insect; thermostable ecdysone receptor; reporter gene;
KW EcR partner protein; USP polypeptide; insect steroid; juvenile hormone;
KW juvenile hormone receptor; ecdysteroid receptor; SRE;
KW steroid response element; beta-galactosidase gene;
KW chloramphenicol acetyltransferase gene; CAT gene; iridoid glycoside;
KW insecticidally-active agent; bisacylhydrazine insecticide; ds.
XX
OS Myzus persicae.
XX
FH Key Location/Qualifiers
FT CDS 1..1353
FT /*tag= a
FT /product= "EcR polypeptide subunit of M. persicae
FT ecdysone receptor"
XX
PN WO9936520-A1.
XX
PD 22-JUL-1999.
XX
PF 15-JAN-1999; 99WO-AU00033.
XX
PR 15-JAN-1998; 98AU-0001356.
XX
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Hannan GN, Hill RJ;
XX
DR WPI; 1999-444393/37.
DR P-PSDB; AAY28606.
XX
PT Steroidal and juvenile hormone receptors and partner proteins,
PT useful for identification of modulators and insecticidal compounds
XX
PS Claim 16; Pages 108-111; 125pp; English.
XX
CC The present sequence is a full-length cDNA encoding an EcR polypeptide
CC subunit of ecdysone receptor from a hemipteran aphid, Myzus
CC persicae. The EcR polypeptide and an EcR partner protein
CC (USP polypeptide) subunits form the functional heterodimeric ecdysone
CC receptor which comprises DNA- and ligand-binding domains and
CC is thermostable. It binds an insect steroid, juvenile hormone
CC or an insecticidally-active agent to form a complex that modulates the
CC expression of a gene operably under the control of a steroid response
CC element (SRE) or a promoter comprising SRE. The polynucleotide is used
CC to produce recombinant insect ecdysone and juvenile hormone receptors
CC which are used to regulate expression of reporter genes like beta-
CC galactosidase, beta-glucuronidase and chloramphenicol acetyltransferase
CC (CAT) genes. The receptors are also useful for screening and identifying
CC insecticidally-active agents e.g. bisacylhydrazine insecticide, iridoid
CC glycoside and other non-steroidal modulators of the ecdysteroid and
CC juvenile hormone receptors.
XX
SQ Sequence 1353 BP; 448 A; 289 C; 310 G; 306 T; 0 other:

Query Match 75.1%; Score 1350; DB 20; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	448	atgtcgaccaaacagctacgaccggtagcgtccatgtggaaaaatcgtaaaagaagag	507
Db	1	atgtcgaccaaacagctacgaccggtagcgtccatgtggaaaaatcgtaaaagaagag	60
Qy	508	ttgtctccgcacaaacagccctgtcgaggactcagcagccattcgatgggttgaagaagaag	567
Db	61	ttgtctccgcacaaacagccctgtcgaggactcagcagccattcgatgggttgaagaagaag	120
Qy	568	aaactcaaccacacgcgcctcgaccggtagtcgtcaacacccctcgatcgcccccgggggt	627
Db	121	aaactcaaccacacgcgcctcgaccggtagtcgtcaacacccctcgatcgcccccgggggt	180

Qy 628 ggcgttggcaatgtgctgaacaaccgaccccccgaagagctgtgcctgggtggc 687
|||
Db 181 ggcgttggcaatgtgctgaacaaccgaccccccgaagagctgtgcctgggtggc 240
|||
Qy 688 gaccggcgccgttaccattacaacacgtctcacatgcaaggatgcaaggggttc 747
|||
Db 241 gaccggcgccgttaccattacaacacgtctcacatgcaaggatgcaaggggttc 300
|||
Qy 748 cggaggagcatcacaagaacgcccgttaccagtgcacatgcgaaatcgaaatc 807
|||
Db 301 cggaggagcatcacaagaacgcccgttaccagtgcacatgcgaaatcgaaatc 360
|||
Qy 808 gacatgtacatgaggcgaaagtgcacaggatgcggctgaaaaatgcctgaccgtcg 867
|||
Db 361 gacatgtacatgaggcgaaagtgcacaggatgcggctgaaaaatgcctgaccgtcg 420
|||
Qy 868 atgaggcctgaatgtttgtacctaagttcaatgcgcgtaaaaaaaaggaaaaaa 927
|||
Db 421 atgaggcctgaatgtttgtacctaagttcaatgcgcgtaaaaaaaaggaaaaaa 480
|||
Qy 928 gctcaacgagaaaaagataaaccattactacagacatttcctgaaataaaaa 987
|||
Db 481 gctcaacgagaaaaagataaaccattactacagacatttcctgaaataaaaa 540
|||
Qy 988 atagaacctacagagatgaagattgaatgtggtaaccatgataatggcacacctatg 1047
|||
Db 541 atagaacctacagagatgaagattgaatgtggtaaccatgataatggcacacctatg 600
|||
Qy 1048 ccgactgtacccatgtgaaaccccttgagttctgaaacaaaaagaactgatccaccgactt 1107
|||
Db 601 ccgactgtacccatgtgaaaccccttgagttctgaaacaaaaagaactgatccaccgactt 660
|||
Qy 1108 gtctattccaggatcaatatgaagctcttagtggaaaaagacatgaaacgttacaata 1167
|||
Db 661 gtctattccaggatcaatatgaagctcttagtggaaaaagacatgaaacgttacaata 720
|||
Qy 1168 aataatcaaaatatggatgaatatgatgaagaaaaacaaagtgcacaccatatcgaaatc 1227
|||
Db 721 aataatcaaaatatggatgaatatgatgaagaaaaacaaagtgcacaccatatcgaaatc 780
|||
Qy 1228 atcactgagatgacaataactcacagttcaactgttgcggccaaacgattacca 1287
|||
Db 781 atcactgagatgacaataactcacagttcaactgttgcggccaaacgattacca 840
|||
Qy 1288 ggttcgataaacttgcataagagaagatcaaacttactcaaggcttgcgtcaagtgaa 1347
|||
Db 841 ggttcgataaacttgcataagagaagatcaaacttactcaaggcttgcgtcaagtgaa 900
|||
Qy 1348 gctatgtatgtcaggtagcaagggatgatgacatcaccactgactcaatagtgtttgt 1407
|||
Db 901 gctatgtatgtcaggtagcaagggatgacatcaccactgactcaatagtgtttgt 960
|||
Qy 1408 aacaaccagccatccatgtcatttgcgttgcataataacaaagctggattggagatgccattgaa 1467
|||
Db 961 aacaaccagccatccatgtcatttgcgttgcataataacaaagctggattggagatgccattgaa 1020
|||
Qy 1468 aaccaactgtcattcagtcgttgcataatgtacaatatgaagggtggataacgcagaatatgcc 1527
|||
Db 1021 aaccaactgtcattcagtcgttgcataatgtacaatatgaagggtggataacgcagaatatgcc 1080
|||
Qy 1528 ttattgaccgcacatgtcataatgtcgttgcgttgcataatgtacaatatgaagggtggataacgcagaatatgcc 1587
|||
Db 1081 ttattgaccgcacatgtcataatgtcgttgcgttgcataatgtacaatatgaagggtggataacgcagaatatgcc 1140
|||
Qy 1588 gagaaaatccaagaatctacacttaggtgcctaaaagcttatgttagataatcgagaccgt 1647
|||
Db 1141 gagaaaatccaagaatctacacttaggtgcctaaaagcttatgttagataatcgagaccgt 1200
|||
Qy 1648 gacacagcaactgtacgatgtcgacttctctcgtacttacagaattgcgcacatta 1707
|||

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Db 1201 gacacagcaactgtacgatatgcgcgacttcttcgtacttacagaattgcgcacatta 1260
Qy 1708 ggcaatggaaaactctgagctatgtatgacactgaaactgaaaaacagagtagtacccca 1767
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||
Db 1261 ggcaatggaaaactctgagctatgtatgacactgaaactgaaaaacagagtagtacccca 1320
Qy 1768 ttcttgccgaaatatggatgtcatgcca 1797
    ||||||| ||||||| ||||||| ||||||| |||||
Db 1321 ttcttgccgaaatatggatgtcatgcca 1350

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SUMMARIES

% Result Query No. Score Match Length DB ID							Description
	1	34	1.9	343	11	BG262692	BG262692 WHE0940_B
c	2	31	1.7	501	10	AV431489	AV431489 AV431489
c	3	29	1.6	342	11	BG263081	BG263081 WHE0946_H
c	4	29	1.6	498	11	BG262509	BG262509 WHE0936_G
	5	29	1.6	531	10	AU066588	AU066588 AU066588
	6	29	1.6	682	13	CNS01UUW	AL168305 Tetraodon
	7	29	1.6	865	13	CNS04VAZ	AL308852 Tetraodon
	8	27	1.5	449	13	L4393X	AL354210 Leishmani
c	9	26	1.4	203	13	AZ605406	AZ605406 IM0426A15
	10	26	1.4	527	10	AV628473	AV628473 AV628473
c	11	26	1.4	828	10	AA986599	AA986599 uc81h02.y
	12	25	1.4	263	10	AA409255	AA409255 EST01178
	13	25	1.4	362	10	AI597416	AI597416 vd86a08.y
	14	25	1.4	364	10	AI020332	AI020332 ub27b01.r
	15	25	1.4	468	13	AQ848107	AQ848107 LMAJFV1_1
	16	25	1.4	494	11	BF450595	BF450595 uz68a05.y
c	17	25	1.4	495	10	AW356009	AW356009 707018D07
c	18	25	1.4	550	10	AW927646	AW927646 945012H02
c	19	25	1.4	562	10	BE129837	BE129837 945030H09
	20	25	1.4	610	10	AW927887	AW927887 945010E03
c	21	25	1.4	616	10	AW129803	AW129803 707004E01
	22	25	1.4	637	10	AW289014	AW289014 707004E01
	23	25	1.4	655	10	BE310176	BE310176 601092815
	24	25	1.4	658	10	AV399810	AV399810 AV399810
	25	25	1.4	659	11	BF124507	BF124507 601761747
	26	25	1.4	696	11	BF784168	BF784168 602108030
	27	25	1.4	722	10	AI326449	AI326449 mm72a03.x
	28	25	1.4	789	11	BI227188	BI227188 602949305
	29	25	1.4	792	11	BF166495	BF166495 601774990
	30	25	1.4	864	10	AV399543	AV399543 AV399543
	31	25	1.4	969	11	BF784421	BF784421 602110804
c	32	25	1.4	1191	10	BE300471	BE300471 600944055
	33	24	1.3	240	10	AV196856	AV196856 AV196856
c	34	24	1.3	289	10	AW028652	AW028652 wv33f12.x
	35	24	1.3	330	10	BE643572	BE643572 945041F03
	36	24	1.3	350	13	AQ903988	AQ903988 GSSTc0582
	37	24	1.3	360	10	BE050736	BE050736 za68h12.b
	38	24	1.3	360	11	C65115	C65115 C65115 Yuji
	39	24	1.3	375	10	AU164151	AU164151 AU164151
	40	24	1.3	378	11	BG943346	BG943346 ax36e09.x
	41	24	1.3	403	11	BE994256	BE994256 UI-M-CG0p
	42	24	1.3	432	11	BF099352	BF099352 601751738
	43	24	1.3	488	10	BE051832	BE051832 za88f12.g
	44	24	1.3	505	10	BE393286	BE393286 601308304
	45	24	1.3	537	10	AV432941	AV432941 AV432941

SEQ ID NO: 9

SUMMARIES

% Result Query No. Score Match Length DB ID							Description
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1	507.4	28.2	2401	3	AF049136	AF049136 Locusta m	
2	460.4	25.6	2469	3	TMECDYREC	Y11533 T.molitor m	
3	382.6	21.3	4562	3	AF034086	AF034086 Celuca pu	
4	341.2	19.0	2355	3	AF325360	AF325360 Calliphor	
5	338.6	18.8	3336	3	LCU75355	U75355 Lucilia cup	
6	315.4	17.6	4130	3	AF210733	AF210733 Aedes alb	
7	312.2	17.4	3875	3	AF020187	AF020187 Amblyomma	
8	310.6	17.3	1812	3	AF020186	AF020186 Amblyomma	
9	310.6	17.3	2166	3	AF020188	AF020188 Amblyomma	
10	307.4	17.1	4158	3	AAU02021	U02021 Aedes aegyp	
11	307.2	17.1	2840	3	MSU19812	U19812 Manduca sex	
12	300.6	16.7	3217	3	CCAJ4341	AJ224341 Ceratitis	
13	298.2	16.6	3962	3	CFU29531	U29531 Choristoneu	
14	298.2	16.6	6852	3	AF092030	AF092030 Choriston	
15	295	16.4	5534	3	DROECR	M74078 Drosophila	
16	273.2	15.2	1934	6	A59201	A59201 Sequence 2	
17	273.2	15.2	2464	6	A59202	A59202 Sequence 3	
18	273.2	15.2	2745	3	HVECR	Y09009 H.virescens	
19	273.2	15.2	2745	6	A59203	A59203 Sequence 4	
c	20	272.6	15.2	8363	12	AF098284	AF098284 Cloning v
	21	272.6	15.2	11001	12	AF264696	AF264696 Cloning v
	22	271.6	15.1	2349	3	S60739	S60739 cEcRH=ecdys
	23	257.8	14.3	2711	3	BMOECDYREC	L35266 Bombyx mori
	24	254	14.1	2720	3	BMOBMECRB1	D43943 Silkworm mR
	25	212.6	11.8	1017	3	PCO251809	AJ251809 Precis co
	26	202.4	11.3	1038	3	BAN251810	AJ251810 Bicyclus
	27	201	11.2	1656	6	AR095098	AR095098 Sequence
	28	188	10.5	948	6	A59205	A59205 Sequence 6
	29	171.4	9.5	8743	2	AC019981	AC019981 Drosophil
	30	171.4	9.5	135182	3	AC007121	AC007121 Drosophil
c	31	171.4	9.5	163990	3	AC009255	AC009255 Drosophil
c	32	171.4	9.5	180699	3	AC008339	AC008339 Drosophil
c	33	171.4	9.5	312373	3	AE003784	AE003784 Drosophil
	34	153.6	8.5	2070	10	RNU18374	U18374 Rattus norv
	35	150.4	8.4	1798	10	MMU09416	U09416 Mus musculu
	36	137.8	7.7	1456	10	MMU09418	U09418 Mus musculu
	37	137.8	7.7	1555	10	MMU09417	U09417 Mus musculu
	38	136.2	7.6	189	3	UPU31817	U31817 Uca pugilat
	39	129.8	7.2	621	3	AF121910	AF121910 Bradyisia
	40	128.8	7.2	2218	9	HSU68233	U68233 Human farne
	41	128.8	7.2	2233	6	I92592	I92592 Sequence 1
	42	121	6.7	546	3	AF239825	AF239825 Sarcophag
	43	120.6	6.7	183	6	E32705	E32705 Novel nucle
	44	115.4	6.4	1431	9	AF384555	AF384555 Homo sapi
	45	110.4	6.1	1524	9	BC008819	BC008819 Homo sapi

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1797	100.0	1797	22	AAF32137	M persicae ecdyson
2	1350	75.1	1353	20	AAX90669	M. persicae ecdyso
3	424.8	23.6	585	20	AAX90668	M. persicae ecdyso
4	424.8	23.6	585	22	AAF32134	M persicae ecdyson
5	333.8	18.6	2812	19	AAV60302	Lucilia cuprina ec
6	326.6	18.2	2273	20	AAX90666	CDNA encoding EcR
7	326.6	18.2	2273	22	AAF32130	L cuprina ecdysone
8	300.2	16.7	2126	21	AAA10312	European corn bore
9	295	16.4	2241	18	AAV06244	Modified ecdysone
10	295	16.4	2970	14	AAQ37556	DHR23alpha cDNA cl
11	295	16.4	5534	12	AAQ13574	EcR gene. Drosoph
12	293.4	16.3	2241	21	AAZ51469	Vector pVgRXR enco
13	293.4	16.3	2295	21	AAZ51470	Vector pVgRXR-5A/5
14	293.4	16.3	2301	21	AAZ51471	Control vector pVg
15	290.8	16.2	3126	18	AAV06245	Modified ecdysone
16	290.2	16.1	2241	18	AAV06243	Modified ecdysone
17	273.2	15.2	1934	18	AAT45793	Heliothis ecdysone
18	273.2	15.2	2464	18	AAT45794	Heliothis ecdysone

19	273.2	15.2	2745	18	AAT45795	Heliothis ecdysone	
20	257.8	14.3	1977	20	AAX07557	Synthetic modified	
21	257.8	14.3	2711	20	AAX07553	Bombyx mori nuclea	
22	257.8	14.3	9072	20	AAX07558	Synthetic modified	
23	201	11.2	1656	19	AAT86658	Ecdysone receptor	
24	201	11.2	1656	19	AAV02768	Drosophila ecdyson	
25	201	11.2	1656	21	AAZ57062	Drosophila ecdyson	
26	201	11.2	1656	21	AAZ92154	Ecdysone receptor	
27	188	10.5	948	18	AAT45796	Spodoptera ecdyson	
28	150.4	8.4	1787	17	AAT31928	Retinoid X recepto	
29	137.8	7.7	1677	17	AAT31932	Retinoid X recepto	
30	128.8	7.2	2233	19	AAV10120	Human retinoid rec	
31	123.2	6.9	936	22	AAF58252	Oligonucleotide D1	
32	123.2	6.9	936	22	AAF58254	Oligonucleotide D1	
33	123.2	6.9	936	22	AAF58257	Oligonucleotide D1	
34	123.2	6.9	936	22	AAF58259	Oligonucleotide D2	
35	123.2	6.9	936	22	AAF58262	Oligonucleotide D2	
36	123.2	6.9	938	22	AAF58255	Oligonucleotide D1	
c	37	121.4	6.8	936	22	AAF58252	Oligonucleotide D1
c	38	121.4	6.8	936	22	AAF58254	Oligonucleotide D1
c	39	121.4	6.8	936	22	AAF58257	Oligonucleotide D1
c	40	121.4	6.8	936	22	AAF58259	Oligonucleotide D2
c	41	121.4	6.8	936	22	AAF58262	Oligonucleotide D2
c	42	121.4	6.8	938	22	AAF58255	Oligonucleotide D1
43	120.6	6.7	183	20	AAX59971	Swellfish ANO23 pr	
44	115.4	6.4	2220	22	AAD12786	Human nuclear horm	
45	110.4	6.1	1528	21	AAZ35043	Human nuclear orph	

ALIGNMENTS

RESULT 1
 AAF32137
 ID AAF32137 standard; cDNA; 1797 BP.
 XX
 AC AAF32137;
 XX
 DT 10-APR-2001 (first entry)
 XX
 DE M persicae ecdysone receptor EcR subunit coding sequence SEQ ID NO: 13.
 XX
 KW Insect; steroid hormone receptor; juvenile hormone receptor; fly;
 KW EcR subunit; USP subunit; insecticide; ss.
 XX
 OS Myzus persicae.
 XX
 PN WO200102436-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-AU00799.
 XX
 PR 01-JUL-1999; 99US-0346470.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Hill RJ, Hannan GN;
 XX
 DR WPI; 2001-080981/09.
 DR P-PSDB; AAB67101.
 XX
 PT New nucleic acid molecule for the regulation of gene expression in
 PT insects -
 XX
 PS Claim 23; Page 138-141; 172pp; English.
 XX
 CC The present invention provides the protein and coding sequences of the
 CC Bemisia tabaci (Silverleaf whitefly), Myzus persicae (aphid) and Lucilia
 CC cuprina (sheep blowfly) steroid and juvenile hormone steroid receptor
 CC subunits EcR and USP. These can be used to screen for agents with

CC insecticidal activity.

XX

SQ Sequence 1797 BP; 512 A; 444 C; 459 G; 382 T; 0 other;

Query Match 100.0%; Score 1797; DB 22; Length 1797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atgatggaccagaaatgtgacgtccgcggtggtgtcgctgtccgcgcggatc 60
||| |||||
Db 1 atgatggaccagaaatgtgacgtccgcggtggtgtcgctgtccgcgcggatc 60
||| |||||
Qy 61 ggtggccgggtgtccgcggcctcatgtcgtaacaaccgtggccgtggccgaccgaggtc 120
||| |||||
Db 61 ggtggccgggtgtccgcggcctcatgtcgtaacaaccgtggccgtggccgaccgaggtc 120
||| |||||
Qy 121 atcatcaaaccgcgttagtccgtccgtggcaggtggccaccgggtggcagtaccacggc 180
||| |||||
Db 121 atcatcaaaccgcgttagtccgtccgtggcaggtggccaccgggtggcagtaccacggc 180
||| |||||
Qy 181 ctgccggccgcctccgacgcgtcatcgcgcaagcccggccaggccggccacttgcggg 240
||| |||||
Db 181 ctgccggccgcctccgacgcgtcatcgcgcaagcccggccaggccggccacttgcggg 240
||| |||||
Qy 241 ccgcagcagcaagtggccgcgtccgcacggctgtttccgcacatcgct 300
||| |||||
Db 241 ccgcagcagcaagtggccgcgtccgcacggctgtttccgcacatcgct 300
||| |||||
Qy 301 ggcgtcaagcgactcaggccgcacgattgggtggccgtcaactcgccgcgcctttcg 360
||| |||||
Db 301 ggcgtcaagcgactcaggccgcacgattgggtggccgtcaactcgccgcgcctttcg 360
||| |||||
Qy 361 cccggcacgtcgcacatatacctacacagtcatatcgAACGGCGGCGGTGGCGGCGGT 420
||| |||||
Db 361 cccggcacgtcgcacatatacctacacagtcatatcgAACGGCGGCGGTGGCGGCGGT 420
||| |||||
Qy 421 ggcggcggtgttacaacacgtctccaatgtcgaccaacagctacgaccgtacagtccg 480
||| |||||
Db 421 ggcggcggtgttacaacacgtctccaatgtcgaccaacagctacgaccgtacagtccg 480
||| |||||
Qy 481 atgagtggaaaaatcgtaaagaagagttgtctccgcacacggctgtcggttcac 540
||| |||||
Db 481 atgagtggaaaaatcgtaaagaagagttgtctccgcacacggctgtcggttcac 540
||| |||||
Qy 541 agccattcgatgggtgaagaagaagaaactcaaccacacgcgcgtcgaccgtgtcg 600
||| |||||
Db 541 agccattcgatgggtgaagaagaagaaactcaaccacacgcgcgtcgaccgtgtcg 600
||| |||||
Qy 601 aacacctcgccatcgccccccccgggggtggcggtggcaatgtgtcgaccaaccgac 660
||| |||||
Db 601 aacacctcgccatcgccccccccgggggtggcggtggcaatgtgtcgaccaaccgac 660
||| |||||
Qy 661 cccgaagagctgtcgccgtgtggcgaccggctgtccgggttaccattacaacgctctc 720
||| |||||
Db 661 cccgaagagctgtcgccgtgtggcgaccggctgtccgggttaccattacaacgctctc 720
||| |||||
Qy 721 acatcgcaaggatgcagggttcttcggaggagcatcaccacggatcgaccgtgtacc 780
||| |||||
Db 721 acatcgcaaggatgcagggttcttcggaggagcatcaccacggatcgaccgtgtacc 780
||| |||||
Qy 781 tgcaagtacggcaacaattgcgaaatcgacatgtacatgaggcggaatgcaggatgc 840
||| |||||
Db 781 tgcaagtacggcaacaattgcgaaatcgacatgtacatgaggcggaatgcaggatgc 840
||| |||||
Qy 841 cggctgaaaaatgcgtaccgtcgcatgaggcgtgaatgtgttgcacatgcggatgc 900
||| |||||
Db 841 cggctgaaaaatgcgtaccgtcgcatgaggcgtgaatgtgttgcacatgcggatgc 900
||| |||||
Qy 901 tgccgactaaaaaaaaggagaaaaagctcaacgagaaaaagataaaccattctact 960
||| |||||

Db 901 tgcgcagtaaaaagaaaaggagaaaaagctcaacgagaaaaagataaaccaaattctact 960
Qy 961 acagacatttctcctgaaataataaaaatagaacctacagagatgaagattgtgg 1020
|||
Db 961 acagacatttctcctgaaataataaaaatagaacctacagagatgaagattgtgg 1020
Qy 1021 gaaccaatgataatgggcacacctatgccgactgtacctacgtgaaacctttagttct 1080
|||
Db 1021 gaaccaatgataatgggcacacctatgccgactgtacctacgtgaaacctttagttct 1080
Qy 1081 gaacaaaagaactgatccaccgacttgttatccaggatcaatatgaagtcctagt 1140
|||
Db 1081 gaacaaaagaactgatccaccgacttgttatccaggatcaatatgaagtcctagt 1140
Qy 1141 gaaaaagacatgaaacgaaaacttaacaataatcaaataatggatgaatgtgatgaagaa 1200
|||
Db 1141 gaaaaagacatgaaacgaaaacttaacaataatcaaataatggatgaatgtgatgaagaa 1200
Qy 1201 aaacaaaagtgcacaccacatatcgaatcatcactgagatgacaataactcacatgtcaactg 1260
|||
Db 1201 aaacaaaagtgcacaccacatatcgaatcatcactgagatgacaataactcacatgtcaactg 1260
Qy 1261 attgttagttgccaaacgattaccagggtttcgataaacttgcataagagaagatcaaatc 1320
|||
Db 1261 attgttagttgccaaacgattaccagggtttcgataaacttgcataagagaagatcaaatc 1320
Qy 1321 actttactcaaggctgtcaagtgaagctatgtatgttcaggtagcaaggaaatgtac 1380
|||
Db 1321 actttactcaaggctgtcaagtgaagctatgtatgttcaggtagcaaggaaatgtac 1380
Qy 1381 atcaccactgactcaatagtgttgctaacaaccagccatccagctgattcatataac 1440
|||
Db 1381 atcaccactgactcaatagtgttgctaacaaccagccatccagctgattcatataac 1440
Qy 1441 aaagctggattggagatgccattgaaaaccaactgtcattcagtcggttatgtacaat 1500
|||
Db 1441 aaagctggattggagatgccattgaaaaccaactgtcattcagtcggttatgtacaat 1500
Qy 1501 atgaaggtagataacgcagaatatgccttattgaccgcatcgtcatatttcgagtagg 1560
|||
Db 1501 atgaaggtagataacgcagaatatgccttattgaccgcatcgtcatatttcgagtagg 1560
Qy 1561 ccaaatttactagatggtagataacgcagaatatgccttattgaccgcatcgtcatatttcgagtagt 1620
|||
Db 1561 ccaaatttactagatggtagataacgcagaatatgccttattgaccgcatcgtcatatttcgagtagt 1620
Qy 1621 aaagcttatgttagataatcgagaccgtgacacagcaactgtacgatgtcgacttctc 1680
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Db 1621 aaagcttatgttagataatcgagaccgtgacacagcaactgtacgatgtcgacttctc 1680
Qy 1681 tcagtagttacagaattgcgcacattaggcaatgaaaactctgagctatgtatgacactg 1740
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Db 1681 tcagtagttacagaattgcgcacattaggcaatgaaaactctgagctatgtatgacactg 1740
Qy 1741 aaactgaaaaacagagtagtaccccttgcgcgaaatatggatgtcatgcca 1797
|||
Db 1741 aaactgaaaaacagagtagtaccccttgcgcgaaatatggatgtcatgcca 1797

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
C	1	171.4	9.5	501	10	AI514995 LD46649.5
	2	171.4	9.5	595	10	AI544194 LD47647.5
	3	150	8.3	917	10	AI987611 ul86d09.y
	4	144.6	8.0	523	10	AI099367 ue30b12.x
	5	140	7.8	851	13	CNS011ME AL100448 Drosophil
	6	137.8	7.7	1728	12	AK002513 Mus muscu

7	135.8	7.6	672	10	AI117017	AI117017 ue30b12.y	
8	131.6	7.3	975	11	BF787802	BF787802 602113568	
9	131	7.3	673	11	BF384905	BF384905 602045211	
10	130	7.2	868	11	BI330645	BI330645 602981090	
11	123.4	6.9	574	10	AI258616	AI258616 LP01848.5	
12	118.8	6.6	652	11	BG710420	BG710420 pg1ln.pk0	
13	115.4	6.4	756	11	BG171220	BG171220 602321423	
14	112	6.2	346	10	AW483842	AW483842 56794 MAR	
c	15	110.4	6.1	578	10	AI831552	AI831552 wj09d10.x
	16	110.4	6.1	891	10	AL558946	AL558946 AL558946
	17	110.4	6.1	1024	10	BE542999	BE542999 601068920
	18	108.8	6.1	612	11	BF385640	BF385640 602045890
	19	108.8	6.1	674	11	BF232668	BF232668 602023254
	20	108.8	6.1	958	11	BF235121	BF235121 602027886
	21	108.6	6.0	640	11	BG423659	BG423659 602449571
	22	107.8	6.0	470	10	AA538642	AA538642 LD18219.5
	23	107.2	6.0	611	11	BG710718	BG710718 pg1ln.pk0
	24	105.6	5.9	358	10	AW431214	AW431214 71543 MAR
	25	105.6	5.9	563	10	BE233303	BE233303 139430 MA
	26	104.4	5.8	277	10	BE755918	BE755918 209807 MA
	27	103.6	5.8	820	10	AL524426	AL524426 AL524426
	28	103.2	5.7	878	10	AL555760	AL555760 AL555760
	29	103.2	5.7	895	10	AL531027	AL531027 AL531027
	30	101.2	5.6	672	13	AZ897361	AZ897361 RPCI-24-2
	31	100.4	5.6	818	13	CNS02CM0	AL191313 Tetraodon
	32	99.8	5.6	1036	13	CNS03YPQ	AL266615 Tetraodon
	33	99.6	5.5	744	11	BG756857	BG756857 602710341
	34	99.6	5.5	870	10	AL516240	AL516240 AL516240
	35	99.6	5.5	902	10	AL521072	AL521072 AL521072
	36	98.4	5.5	861	11	BI261066	BI261066 602972272
	37	98.2	5.5	965	11	BE902332	BE902332 601675628
	38	98	5.5	718	11	BF569478	BF569478 602185964
	39	97.6	5.4	717	10	AU135617	AU135617 AU135617
	40	97.4	5.4	554	11	BI149124	BI149124 602913931
	41	96	5.3	765	11	BI146133	BI146133 602910928
	42	96	5.3	962	13	CNS02JSQ	AL200627 Tetraodon
	43	95.4	5.3	841	10	AL559175	AL559175 AL559175
	44	94.8	5.3	643	10	AV655930	AV655930 AV655930
c	45	94.6	5.3	832	13	CNS013QT	AL103199 Drosophil

67346470

Sequence Comparison A

RESULT 2
O02035
ID O02035 PRELIMINARY; PRT; 491 AA.
AC O02035;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ECDYSONE RECEPTOR.
GN ECR.
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98000286; PubMed=9342239;
RA Mouillet J.F., Delbecque J.P., Quennedey B., Delachambre J.;
RT "Cloning of two putative ecdysteroid receptor isoforms from *Tenebrio molitor* and their developmental expression in the epidermis during metamorphosis.";
RL Eur. J. Biochem. 248:856-863 (1997).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: TO C4-TYPE STEROID RECEPTOR ZINC FINGER FAMILY.
DR EMBL; Y11533; CAA72296.1; -.
DR HSSP; P20393; 1A6Y.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR000504; RRM.
DR InterPro; IPR001723; Strdhormone_receptor.
DR InterPro; IPR001628; zf-C4.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECECTOR; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 491 AA; 56096 MW; F997E90A56A789D1 CRC64;

Adm. 3

Query Match 45.5%; Score 1434.5; DB 5; Length 491;
Best Local Similarity 65.8%; Pred. No. 8.4e-99;
Matches 293; Conservative 48; Mismatches 51; Indels 53; Gaps 9;

Qy 453 FRVARKYDITTD SIVFANNQPFSADS YNKAGLGDAIENQLSFSRFM YNMKVDNAEYALLT 512
||:||:||: :|||:| |||: |||| ||:||:||:|||:|||:|||:
Db 343 FRMARRYDVQS DSI LFVN NQP YPRDSYNLAGMGETIEDLLHFCRTMYS MKVDNAEYALLT 402
||:||:||:||:||:||:||:||:||:||:||:||:||:
Qy 513 AIVIFSSRPNLLDGW KVEKI QEIY LESLKAYVNDRDTATVRYARLLSVLTELRTLGNE 572
||:||:||:||:||:||:||:||:||:||:||:||:
Db 403 AIVIFSERPSLIEGW KVEKI QEIY LEALRAYVNRRSPSRGTIFAKLLSVLTELRTLG NQ 462
||:||:||:||:||:||:||:||:
Qy 573 NSEL CMTLKLKNR VVPPFLAEIWDV 597
||:||:||:||:||:||:||:
Db 463 NSEM CISLKLKNKKLPPFLDEIWDV 487

Sequence Comparison B

RESULT 2
TMECDYREC
LOCUS TMECDYREC 2469 bp mRNA INV 14-OCT-1997
DEFINITION T.molitor mRNA for ecdysone receptor.
ACCESSION Y11533
VERSION Y11533.1 GI:2155007
KEYWORDS ecdysone receptor; EcR gene.
SOURCE yellow mealworm.
ORGANISM Tenebrio molitor
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tenebrio.
REFERENCE 1 (bases 1 to 2469)
AUTHORS Mouillet, J.F., Delbecque, J.P., Quennedey, B. and Delachambre, J.
TITLE Cloning of two putative ecdysteroid receptor isoforms from Tenebrio molitor and their developmental expression in the epidermis during metamorphosis
JOURNAL Eur. J. Biochem. 248 (3), 856-863 (1997)
MEDLINE 98000286
REFERENCE 2 (bases 1 to 2469)
AUTHORS Mouillet, J.F.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-1997) J.F. Mouillet, Lab Zoologie-CNRS UMR 5548, Faculte des Sciences Gabriel, 6BD Gabriel, 21000 Dijon, France
FEATURES Location/Qualifiers
source 1..2469 /organism="Tenebrio molitor" /db_xref="taxon:7067"
gene 838..2313 /gene="EcR"
CDS 838..2313 /gene="EcR" /codon_start=1 /product="ecdysone receptor" /protein_id="CAA72296.1" /db_xref="GI:2155008" /db_xref="SPTRREMBL:O02035" /translation="MKRRWSQLQAVRVTPEESSSEVTSSSTLVMSPANSLASTDIDGVDLEFWDLNLNGAKSRQRTHYSKRIWPGHTIIASNHHLAKSDTSSMSGREDLSPSSLNGYSADSCDSKKKGPTPRQQEELCLVCGDRASGYHYNALTCEGCKGFRRSITKNAVYQCKYGNNEIDMYMRRKCQECLKKCLSGVMRPECVVPEVQCAVKRKEKKAQKEKDKNPNTTNGSPDVKIEPELSDSEKTLTNGRNRRNISPEQEELILIHRLVYFQNEYEHPSVEDVCRINQPIDGEDQCEIRFRHTTEITILTQVLIVEFAKRLPGFDKLLQEDQIALLKACSSSEMMFRMARRYDVQSDSLIFVNQPYPRDSYVLAGMGETIEDLLHFCRTMYSMKVDNAEYALLTAIVFSERPSLIEGWKVEKIQEYILEALRAYVDNRRSPSRGTIFAKLLSVLTELRTLGNQNQNSEMCISLKLKNKKLPPFLDEIWDVLDKA"
BASE COUNT 682 a 589 c 642 g 556 t
ORIGIN

Query Match 25.6%; Score 460.4; DB 3; Length 2469;
 Best Local Similarity 64.4%; Pred. No. 1e-79;
 Matches 742; Conservative 0; Mismatches 371; Indels 39; Gaps 2;

Qy 640 aatgtgctgaacaaccgacacctcccgaaagagactgtgcctgggtgtggcaccggcgtcc 699
 ||| ||| |||| | |||| | |||| | ||| |||| | |||| | |||| | |||| | |||| |
 Db 1186 AAAGGTCCGACGCCCTCGACAACAGGAAGAATTATGTTGGTGTGGAGACAGAGCGTCC 1245

Qy 700 ggtttaccattacaacgcgtctcacatgcgaaggatgcaggggttcttcggaggagcatc 759
 ||||||| |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
 Db 1246 GGTTACCATTACAACGCATTGACTTGCAGGGTTGCAAAGGTTCTTCAGACCGCAGTATA 1305

Qy 760 accaagaacgccgttaccagtgcagaatgcggcaacaattgcgaaatcgacatgtacatg 819
 ||| |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
 Db 1306 ACAAAAGAACGCTGTGTATCAATGCAAATACGGAAACAATTGCGAAATAGACATGTATATG 1365

